CLAIMS

What is claimed is:

1. A method for the expression of a coding region of interest in a C1 metabolizing bacteria comprising:

a) providing a transformed C1 metabolizing bacterial cell having a chimeric gene comprising;

1) a promoter region of a gene selected from the group consisting of: a *nrtA* gene and a *glnB* gene; and

2) a coding region of interest expressible in a C1 metabolizing bacteria;

wherein the promoter region is operably linked to a coding region of interest; and

b) growing the transformed C1 metabolizing bacteria cell of step (a) in the presence of nitrate wherein the chimeric gene is expressed.

2. A method for the expression of a coding region of interest in a C1 metabolizing bacteria comprising:

a) providing a transformed C1 metabolizing bacterial cell having a chimeric gene comprising;

1) a promoter region of a *glyoxII* gene; and

2) a coding region of interest expressible in a C1 metabolizing bacteria;

wherein the promoter region is operably linked to a coding region of interest; and

b) growing the transformed C1 metabolizing bacteria cell of step (a) at a pH of about 5.5 wherein the chimeric gene is expressed.

3. A method for the expression of a coding region of interest in a C1 metabolizing bacteria comprising:

a) providing a transformed C1 metabolizing bacterial cell having a chimeric gene comprising;

1) a promoter region of a *htpG* gene; and

2) a coding region of interest expressible in a C1 metabolizing bacteria;

wherein the promoter region is operably linked to a coding region of interest; and

b) growing the transformed C1 metabolizing bacteria cell of step (a) at a temperature suitable for induction of the promoter region wherein the chimeric gene is expressed.

4. A method for the expression of a coding region of interest in a C1 metabolizing bacteria comprising:

a) providing a transformed C1 metabolizing bacterial cell having a chimeric gene comprising;

1) a promoter region of a gene selected from the group consisting of: a *moxF* gene and a *hps* gene; and

2) a coding region of interest expressible in a C1 metabolizing bacteria;

wherein the promoter region is operably linked to a coding region of interest; and

b) growing the transformed C1 metabolizing bacteria cell of step (a) in the presence of a C1 carbon source selected from the group consisting of methane and methanol wherein the chimeric gene of step (a) is expressed.

5. A method according to any of Claims 1-4 wherein the C1 metabolizing bacterial host cell is selected from the group consisting of methanotrophs and methylotrophs.

6. A method according to Claim 5 wherein the C1 metabolizing bacterial host cell is a methylotroph selected from the group consisting of *Methylomonas, Methylobacter, Mehtylococcus, Methylosinus, Methylocyctis, Methylomicrobium, Methanomonas, Methylophilus, Methylobacillus, Methylobacterium, Hyphomicrobium, Xanthobacter, Bacillus, Paracoccus, Nocardia, Arthrobacter, Rhodopseudomonas,* and *Pseudomonas.*

7. A method according to Claim 1 wherein the promoter region has the nucleic acid sequence selected from the group consisting of SEQ ID NO:3 and SEQ ID NO:6.

8. A method according to Claim 2 wherein the promoter region has the nucleic acid sequence as set forth in SEQ ID NO:9.

9. A method according to Claim 3 wherein the promoter region has the nucleic acid sequence as set forth in SEQ ID NO:12.

10. A method according to Claim 3 wherein the temperature suitable for induction of the promoter region is selected from the group consisting of:

a) 41-42°C wherein the C1 metabolizing bacteria is mesophilic; and

b) 47-50°C wherein the C1 metabolizing bacteria, is thermophilic

11. A method according to Claim 4 wherein the nucleic acid fragment comprising the promoter region has the nucleic acid sequence selected from the group consisting of SEQ ID NO:15, and 18.

12. A method according to Claim 1 wherein the concentration of nitrate is from about 5mM to about 15mM.

13. The method according to any one of Claims 1 – 4 wherein the coding region of interest is selected from the group consisting of genes encoding: transaldolase, fructose bisphosphate aldolase, keto deoxy phosphogluconate aldolase, phosphoglucomutase, glucose-6-phosphate isomerase, phosphofructokinase, 6-phosphogluconate dehydratase, 6-phosphogluconate-6-phosphate-1 dehydrogenase, *dxs, dxr, ispA, ispD, ispE, ispF, crtE, crtX, crtY, crtI, crtB, crtZ, crtD, crtO, crtW,* genes encoding limonene synthase, *ugp, gumD, wza, espB, espM, waaE, espV, gumH,* genes encoding glycosyltransferase genes, *aroG, aroB, aroQ, aroE*, *aroK*, 5-enolpyruvylshikimate-3-phosphate synthase, *aroC*, *trpE*, *trpD*, *trpC* , *trpB*, *pheA*, *tyrAc, pds, phaC, phaE, efe, pdc, adh*, pinene synthase, bornyl synthase, phellandrene synthase, cineole synthase, sabinene synthase, and taxadiene synthase.

14. A method for the production of zeaxanthin comprising:

a) providing a transformed C1 metabolizing host cell comprising:

1) suitable levels of b-Carotene; and

2) a chimeric gene comprising the promoter region of the *hps* gene operably linked to a coding region encoding β-carotene hydroxylase; and

(b) contacting the host cell of step (a) under suitable growth conditions with an effective amount of a C1 carbon substrate whereby an zeaxanthin is produced.

15. An isolated nucleic acid molecule encoding a nitrate inducible gene selected from the group consisting of:

(a) an isolated nucleic acid molecule encoding the amino acid sequence selected from the group consisting of SEQ ID NO:2 and SEQ ID NO:5;

(b) an isolated nucleic acid molecule that hybridizes with (a) under stringent conditions and is washed with 0.1X SSC, 0.1% SDS, 65°C; or

an isolated nucleic acid molecule that is complementary to (a), or (b).

16. The isolated nucleic acid molecule of Claim 15 selected from the group consisting of SEQ ID NO:1 and SEQ ID NO:4.

17. A polypeptide encoded by the isolated nucleic acid molecule of Claim 15.

18. The polypeptide of Claim 17 selected from the group consisting of SEQ ID NO:2 and SEQ ID NO:5.

19. An isolated nucleic acid molecule comprising a first nucleotide sequence encoding a nrtA enzyme of at least 464 amino acids that has at least 70% identity based on the Smith-Waterman method of alignment when compared to a polypeptide having the sequence as set forth in SEQ ID NO:2;

or a second nucleotide sequence comprising the complement of the first nucleotide sequence.

20. An isolated nucleic acid molecule comprising a first nucleotide sequence encoding a glnB enzyme of at least 112 amino acids that has at least 76% identity based on the Smith-Waterman method of alignment when compared to a polypeptide having the sequence as set forth in SEQ ID NO:5;

or a second nucleotide sequence comprising the complement of the first nucleotide sequence.

21. An isolated nucleic acid molecule encoding a pH inducible gene selected from the group consisting of:

a) an isolated nucleic acid molecule encoding the amino acid sequence as set forth in SEQ ID NO:8;

b) an isolated nucleic acid molecule that hybridizes with (a) under stringent conditions and is washed with 0.1X SSC, 0.1% SDS, 65°C; or

an isolated nucleic acid molecule that is complementary to (a), or (b).

22. The isolated nucleic acid molecule of Claim 21 as set forth in SEQ ID NO:7.

23. A polypeptide encoded by the isolated nucleic acid molecule of Claim 21.

24. The polypeptide of Claim 23 having the amino acid seqeunce as set forth in SEQ ID NO:8.

25. An isolated nucleic acid molecule comprising a first nucleotide sequence encoding a glyoxII enzyme of at least 231 amino acids that has at least 70% identity based on the Smith-Waterman method of alignment when compared to a polypeptide having the sequence as set forth in SEQ ID NO:8;

or a second nucleotide sequence comprising the complement of the first nucleotide sequence.

26. An isolated nucleic acid molecule encoding a temperature inducible gene selected from the group consisting of:

a) an isolated nucleic acid molecule encoding the amino acid sequence as set forth in SEQ ID NO:11;

b) an isolated nucleic acid molecule that hybridizes with (a) under stringent conditions and is washed with 0.1X SSC, 0.1% SDS, 65°C; or an isolated nucleic acid molecule that is complementary to (a), or (b).

27. The isolated nucleic acid molecule of Claim 26 as set forth in SEQ ID NO:10.

28. A polypeptide encoded by the isolated nucleic acid molecule of Claim 26.

29. The polypeptide of Claim 28 having the amino acid sequence as set forth in SEQ ID NO:11.

30. An isolated nucleic acid molecule comprising a first nucleotide sequence encoding a htpG enzyme of at least 644 amino acids that has at least 70% identity based on the Smith-Waterman method of alignment when compared to a polypeptide having the sequence as set forth in SEQ ID NO:11;

or a second nucleotide sequence comprising the complement of the first nucleotide sequence.

31. An isolated nucleic acid molecule encoding a methane or methanol inducible gene selected from the group consisting of:

(a) an isolated nucleic acid molecule encoding the amino acid sequence selected from the group consisting of SEQ ID NO:14, and 17;

(b) an isolated nucleic acid molecule that hybridizes with (a) under stringent conditions and is washed with 0.1X SSC,

0.1% SDS, 65°C; or an isolated nucleic acid molecule that is complementary to (a), or (b).

32. The isolated nucleic acid molecule of Claim 31 selected from the group consisting of SEQ ID NO:13, and 16.

33. A polypeptide encoded by the isolated nucleic acid molecule of Claim 31.

34. The polypeptide of Claim 33 selected from the group consisting of SEQ ID NO:14, and 17.

35. An isolated nucleic acid molecule comprising a first nucleotide sequence encoding a moxF enzyme of at least 89 amino acids that has at least 70% identity based on the Smith-Waterman method of alignment when compared to a polypeptide having the sequence as set forth in SEQ ID NO:14;

or a second nucleotide sequence comprising the complement of the first nucleotide sequence.

36. An isolated nucleic acid molecule comprising a first nucleotide sequence encoding a hps enzyme of at least 215 amino acids that has at least 70% identity based on the Smith-Waterman method of alignment when compared to a polypeptide having the sequence as set forth in SEQ ID NO:17;

or a second nucleotide sequence comprising the complement of the first nucleotide sequence.

37. A promoter region responsive to the presence of nitrate having the nucleic acid sequence selected from the group consisting of SEQ ID NO:3 and SEQ ID NO:6.

38. A promoter region responsive to acidic pH having the nucleic acid sequence as set forth in SEQ ID NO:9.

39. A promoter region responsive to elevated temperatures having the nucleic acid sequence as set forth in SEQ ID NO:12.

40. A promoter region highly expressed in the presence of methane or methanol having the nucleic acid sequence selected from the group consisting of SEQ ID NO:15, and SEQ ID NO:18.